METHOD AND SYSTEM FOR RAPID BIOMOLECULAR RECOGNITION OF AMINO ACIDS AND PROTEIN SEQUENCING

ABSTRACT OF THE DISCLOSURE

[463] Methods, compositions, kits, and apparatus are provided wherein the aminoacyl-tRNA synthetase system is used to analyze amino acids. The method allows very small devices for quantitative or semi-quantitative analysis of the amino acids in samples or in sequential or complete proteolytic digestions. The methods can be readily applied to the detection and/or quantitation of one or more primary amino acids by using cognate aminoacyl-tRNA synthetase and cognate tRNA. The basis of the method is that each of the 20 synthetases and/or a tRNA specific for a different amino acid is separated spatially or differentially labeled. The reactions catalyzed by all 20 synthetases may be monitored simultaneously, or nearly simultaneously, or in parallel. Each separately positioned synthetase or tRNA will signal its cognate amino acid. The synthetase reactions can be monitored using continuous spectroscopic assays. Alternatively, since elongation factor Tu:GTP (EF-Tu:GTP) specifically binds all AA-tRNAs, the aminoacylation reactions catalyzed by the synthetases can be monitored using ligand assays. Microarrays and microsensors for amino acid analysis are provided. Additionally, amino acid analysis devices are integrated with protease digestions to produce miniaturized enzymatic sequenators capable of generating either N- or C-terminal sequence and composition data for a protein or peptide. The possibility of parallel processing of many samples in an automated manner is discussed.